

EX03-083C-USpatentin.txt  
SEQUENCE LISTING

&lt;110&gt; EXELIXIS, INC.

&lt;120&gt; MRACs AS MODIFIERS OF THE RAC PATHWAY AND METHODS OF USE

&lt;130&gt; EX03-083C-US

&lt;150&gt; US 60/428,874

&lt;151&gt; 2002-11-25

&lt;160&gt; 8

&lt;170&gt; PatentIn version 3.2

&lt;210&gt; 1

&lt;211&gt; 1677

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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Lys Met Glu Ile Leu Tyr Ile Leu Val Pro Ser Val Ala Ile Pro Leu  
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Ala Ile Ala Leu Leu Phe Phe Ile Cys Val Cys Arg Asn Asn Gln  
420 425 430

Lys Ser Ser Ser Ala Pro Val Gln Arg Gln Pro Lys His Val Arg Gly  
435 440 445

Gln Asn Val Glu Met Ser Met Leu Asn Ala Tyr Lys Pro Lys Ser Lys  
450 455 460

Ala Lys Glu Leu Pro Leu Ser Ala Val Arg Phe Met Glu Glu Leu Gly  
465 470 475 480

Glu Cys Ala Phe Gly Lys Ile Tyr Lys Gly His Leu Tyr Leu Pro Gly  
485 490 495

Met Asp His Ala Gln Leu Val Ala Ile Lys Thr Leu Lys Asp Tyr Asn  
500 505 510

Asn Pro Gln Gln Trp Met Glu Phe Gln Gln Glu Ala Ser Leu Met Ala  
515 520 525

Glu Leu His His Pro Asn Ile Val Cys Leu Leu Gly Ala Val Thr Gln  
530 535 540

Glu Gln Pro Val Cys Met Leu Phe Glu Tyr Ile Asn Gln Gly Asp Leu  
545 550 555 560

His Glu Phe Leu Ile Met Arg Ser Pro His Ser Asp Val Gly Cys Ser  
565 570 575

Ser Asp Glu Asp Gly Thr Val Lys Ser Ser Leu Asp His Gly Asp Phe  
580 585 590

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Leu His Ile Ala Ile Gln Ile Ala Ala Gly Met Glu Tyr Leu Ser Ser  
595 600 605

His Phe Phe Val His Lys Asp Leu Ala Ala Arg Asn Ile Leu Ile Gly  
610 615 620

Glu Gln Leu His Val Lys Ile Ser Asp Leu Gly Leu Ser Arg Glu Ile  
625 630 635 640

Tyr Ser Ala Asp Tyr Tyr Arg Val Gln Ser Lys Ser Leu Leu Pro Ile  
645 650 655

Arg Trp Met Pro Pro Glu Ala Ile Met Tyr Gly Lys Phe Ser Ser Asp  
660 665 670

Ser Asp Ile Trp Ser Phe Gly Val Val Leu Trp Glu Ile Phe Ser Phe  
675 680 685

Gly Leu Gln Pro Tyr Tyr Gly Phe Ser Asn Gln Glu Val Ile Glu Met  
690 695 700

Val Arg Lys Arg Gln Leu Leu Pro Cys Ser Glu Asp Cys Pro Pro Arg  
705 710 715 720

Met Tyr Ser Leu Met Thr Glu Cys Trp Asn Glu Ile Pro Ser Arg Arg  
725 730 735

Pro Arg Phe Lys Asp Ile His Val Arg Leu Arg Ser Trp Glu Gly Leu  
740 745 750

Ser Ser His Thr Ser Ser Thr Thr Pro Ser Gly Gly Asn Ala Thr Thr  
755 760 765

Gln Thr Thr Ser Leu Ser Ala Ser Pro Val Ser Asn Leu Ser Asn Pro  
770 775 780

Arg Tyr Pro Asn Tyr Met Phe Pro Ser Gln Gly Ile Thr Pro Gln Gly  
785 790 795 800

Gln Ile Ala Gly Phe Ile Gly Pro Pro Ile Pro Gln Asn Gln Arg Phe  
805 810 815

Ile Pro Ile Asn Gly Tyr Pro Ile Pro Pro Gly Tyr Ala Ala Phe Pro  
820 825 830

Ala Ala His Tyr Gln Pro Thr Gly Pro Pro Arg Val Ile Gln His Cys  
835 840 845

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Pro Pro Pro Lys Ser Arg Ser Pro Ser Ser Ala Ser Gly Ser Thr Ser  
850 855 860

Thr Gly His Val Thr Ser Leu Pro Ser Ser Gly Ser Asn Gln Glu Ala  
865 870 875 880

Asn Ile Pro Leu Leu Pro His Met Ser Ile Pro Asn His Pro Gly Gly  
885 890 895

Met Gly Ile Thr Val Phe Gly Asn Lys Ser Gln Lys Pro Tyr Lys Ile  
900 905 910

Asp Ser Lys Gln Ala Ser Leu Leu Gly Asp Ala Asn Ile His Gly His  
915 920 925

Thr Glu Ser Met Ile Ser Ala Glu Leu  
930 935

<210> 8  
<211> 943  
<212> PRT  
<213> Homo sapiens

<400> 8

Met Ala Arg Gly Ser Ala Leu Pro Arg Arg Pro Leu Leu Cys Ile Pro  
1 5 10 15

Ala Val Trp Ala Ala Ala Leu Leu Leu Ser Val Ser Arg Thr Ser  
20 25 30

Gly Glu Val Glu Val Leu Asp Pro Asn Asp Pro Leu Gly Pro Leu Asp  
35 40 45

Gly Gln Asp Gly Pro Ile Pro Thr Leu Lys Gly Tyr Phe Leu Asn Phe  
50 55 60

Leu Glu Pro Val Asn Asn Ile Thr Ile Val Gln Gly Gln Thr Ala Ile  
65 70 75 80

Leu His Cys Lys Val Ala Gly Asn Pro Pro Pro Asn Val Arg Trp Leu  
85 90 95

Lys Asn Asp Ala Pro Val Val Gln Glu Pro Arg Arg Ile Ile Ile Arg  
100 105 110

Lys Thr Glu Tyr Gly Ser Arg Leu Arg Ile Gln Asp Leu Asp Thr Thr  
115 120 125

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Asp Thr Gly Tyr Tyr Gln Cys Val Ala Thr Asn Gly Met Lys Thr Ile  
130 135 140

Thr Ala Thr Gly Val Leu Phe Val Arg Leu Gly Pro Thr His Ser Pro  
145 150 155 160

Asn His Asn Phe Gln Asp Asp Tyr His Glu Asp Gly Phe Cys Gln Pro  
165 170 175

Tyr Arg Gly Ile Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Ile Tyr  
180 185 190

Val Asp Ser Leu Gln Met Gln Gly Glu Ile Glu Asn Arg Ile Thr Ala  
195 200 205

Ala Phe Thr Met Ile Gly Thr Ser Thr His Leu Ser Asp Gln Cys Ser  
210 215 220

Gln Phe Ala Ile Pro Ser Phe Cys His Phe Val Phe Pro Leu Cys Asp  
225 230 235 240

Ala Arg Ser Arg Thr Pro Lys Pro Arg Glu Leu Cys Arg Asp Glu Cys  
245 250 255

Glu Val Leu Glu Ser Asp Leu Cys Arg Gln Glu Tyr Thr Ile Ala Arg  
260 265 270

Ser Asn Pro Leu Ile Leu Met Arg Leu Gln Leu Pro Lys Cys Glu Ala  
275 280 285

Leu Pro Met Pro Glu Ser Pro Asp Ala Ala Asn Cys Met Arg Ile Gly  
290 295 300

Ile Pro Ala Glu Arg Leu Gly Arg Tyr His Gln Cys Tyr Asn Gly Ser  
305 310 315 320

Gly Met Asp Tyr Arg Gly Thr Ala Ser Thr Thr Lys Ser Gly His Gln  
325 330 335

Cys Gln Pro Trp Ala Leu Gln His Pro His Ser His His Leu Ser Ser  
340 345 350

Thr Asp Phe Pro Glu Leu Gly Gly His Ala Tyr Cys Arg Asn Pro  
355 360 365

Gly Gly Gln Met Glu Gly Pro Trp Cys Phe Thr Gln Asn Lys Asn Val

370

375

380

Arg Met Glu Leu Cys Asp Val Pro Ser Cys Ser Pro Arg Asp Ser Ser  
385 390 395 400

Lys Met Gly Ile Leu Tyr Ile Leu Val Pro Ser Ile Ala Ile Pro Leu  
405 410 415

Val Ile Ala Cys Leu Phe Phe Leu Val Cys Met Cys Arg Asn Lys Gln  
420 425 430

Lys Ala Ser Ala Ser Thr Pro Gln Arg Arg Gln Leu Met Ala Ser Pro  
435 440 445

Ser Gln Asp Met Glu Met Pro Leu Ile Asn Gln His Lys Gln Ala Lys  
450 455 460

Leu Lys Glu Ile Ser Leu Ser Ala Val Arg Phe Met Glu Glu Leu Gly  
465 470 475 480

Glu Asp Arg Phe Gly Lys Val Tyr Lys Gly His Leu Phe Gly Pro Ala  
485 490 495

Pro Gly Glu Gln Thr Gln Ala Val Ala Ile Lys Thr Leu Lys Asp Lys  
500 505 510

Ala Glu Gly Pro Leu Arg Glu Glu Phe Arg His Glu Ala Met Leu Arg  
515 520 525

Ala Arg Leu Gln His Pro Asn Val Val Cys Leu Leu Gly Val Val Thr  
530 535 540

Lys Asp Gln Pro Leu Ser Met Ile Phe Ser Tyr Cys Ser His Gly Asp  
545 550 555 560

Leu His Glu Phe Leu Val Met Arg Ser Pro His Ser Asp Val Gly Ser  
565 570 575

Thr Asp Asp Asp Arg Thr Val Lys Ser Ala Leu Glu Pro Pro Asp Phe  
580 585 590

Val His Leu Val Ala Gln Ile Ala Ala Gly Met Glu Tyr Leu Ser Ser  
595 600 605

His His Val Val His Lys Asp Leu Ala Thr Arg Asn Val Leu Val Tyr  
610 615 620

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Asp Lys Leu Asn Val Lys Ile Ser Asp Leu Gly Leu Phe Arg Glu Val  
625 630 635 640

Tyr Ala Ala Asp Tyr Tyr Lys Leu Leu Gly Asn Ser Leu Leu Pro Ile  
645 650 655

Arg Trp Met Ala Pro Glu Ala Ile Met Tyr Gly Lys Phe Ser Ile Asp  
660 665 670

Ser Asp Ile Trp Ser Tyr Gly Val Val Leu Trp Glu Val Phe Ser Tyr  
675 680 685

Gly Leu Gln Pro Tyr Cys Gly Tyr Ser Asn Gln Asp Val Val Glu Met  
690 695 700

Ile Arg Asn Arg Gln Val Leu Pro Cys Pro Asp Asp Cys Pro Ala Trp  
705 710 715 720

Val Tyr Ala Leu Met Ile Glu Cys Trp Asn Glu Phe Pro Ser Arg Arg  
725 730 735

Pro Arg Phe Lys Asp Ile His Ser Arg Leu Arg Ala Trp Gly Asn Leu  
740 745 750

Ser Asn Tyr Asn Ser Ser Ala Gln Thr Ser Gly Ala Ser Asn Thr Thr  
755 760 765

Gln Thr Ser Ser Leu Ser Thr Ser Pro Val Ser Asn Val Ser Asn Ala  
770 775 780

Arg Tyr Val Gly Pro Lys Gln Lys Ala Pro Pro Phe Pro Gln Pro Gln  
785 790 795 800

Phe Ile Pro Met Lys Gly Gln Ile Arg Pro Met Val Pro Pro Pro Gln  
805 810 815

Leu Tyr Val Pro Val Asn Gly Tyr Gln Pro Val Pro Ala Tyr Gly Ala  
820 825 830

Tyr Leu Pro Asn Phe Tyr Pro Val Gln Ile Pro Met Gln Met Ala Pro  
835 840 845

Gln Gln Val Pro Pro Gln Met Val Pro Lys Pro Ser Ser His His Ser  
850 855 860

Gly Ser Gly Ser Thr Ser Thr Gly Tyr Val Thr Thr Ala Pro Ser Asn  
865 870 875 880

EX03-083C-USpatentin.txt

Thr Ser Met Ala Asp Arg Ala Ala Leu Leu Ser Glu Gly Ala Asp Asp  
885 890 895

Thr Gln Asn Ala Pro Glu Asp Gly Ala Gln Ser Thr Val Gln Glu Ala  
900 905 910

Glu Glu Glu Glu Glu Gly Ser Val Pro Glu Thr Glu Leu Leu Gly Asp  
915 920 925

Cys Asp Thr Leu Gln Val Asp Glu Ala Gln Val Gln Leu Glu Ala  
930 935 940